Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. (currently amended) A method of analyzing a target nucleic acid, comprising:

(a) designing an array of probes based on a known reference sequence, the array comprising a probe set comprising probes complementary to and spanning the known reference sequence, the probes immobilized on at least one support;

(b) hybridizing the target nucleic acid to the array of probes, wherein the target nucleic acid has a sequence which is a variant of the reference sequence and provided the array of probes does not contain every possible probe sequence of a given length;

(c) determining relative hybridization of the probes to the target nucleic acid,

(d) estimating the sequence of the target nucleic acid from the relative hybridization of the probes;

(e) designing a further array of probes based on the estimated sequence obtained in step (d), the further array comprising a probe set comprising probes complementary to and spanning the estimated sequence of the target nucleic acid, the probes immobilized on at least one support and provided the further probe array does not contain every possible probe sequence of a given length;

(f) hybridizing the target nucleic acid to the further array of probes;

(g) determining the relative hybridization of the probes of the further array to the target nucleic acid;

(h) reestimating the sequence of the target nucleic acid from the relative hybridization of the probes of the further array.

2. (previously presented) The method of claim 1, further comprising repeating steps (e)-(h) as necessary until the reestimated sequence of the target nucleic acid is constant between successive cycles.

3. (original) The method of claim 1, wherein the target nucleic acid is a species variant of the reference sequence.

4. (original) The method of claim 1, wherein the reference sequence is from a human and the target nucleic acid is from a primate.

5. (original) The method of claim 1, wherein the target nucleic acid shows 50-99% sequence identity with the reference sequence.

6. (original) The method of claim 1, wherein the target nucleic acid shows 80-95% sequence identity with the reference sequence.

7. (original) The method of claim 1, wherein the reference sequence is at least 1000 nucleotides long, the array comprises a probe set comprising overlapping probes that are perfectly complementary to and span the reference sequence, and the further array comprises probes that are perfectly complementary to and span the estimated sequence.

8. (previously presented) The method of claim 1, wherein an estimated sequence of the target nucleic acid includes a nucleotide whose identity is ambiguous and the probe set showing perfect complementarity to the estimated sequence includes a probe having a pooled nucleotide aligned with the position of ambiguity in the target sequence.

9. (original) The method of claim 1, wherein the reference sequence is at least 10 kb.

10. (original) The method of claim 1, wherein the reference sequence is at least 1000 kb.

11. (previously presented) The method of claim 1, wherein the reference sequence includes at least 90% of the human genome and a plurality of arrays and further arrays are designed in steps (a) and (f) respectively.

12. (original) The method of claim 1, wherein the array of probes comprises:

(1) a first probe set comprising a plurality of probes, each probe comprising a segment of at least six nucleotides exactly complementary to a subsequence of the reference sequence, the segment including at least one interrogation position complementary to a corresponding nucleotide in the reference sequence,

(2) second, third and fourth probe sets, each comprising a corresponding probe for each probe in the first probe set, the probes in the second, third and fourth probe sets being identical to a sequence comprising the corresponding probe from the first probe set or a subsequence of at least six nucleotides thereof that includes the at least one interrogation position, except that the at least one interrogation position is occupied by a different nucleotide in each of the four corresponding probes from the four probe sets.

13. (original) The method of claim 12, wherein the sequence of the target nucleic acid is estimated by:

(a) comparing the relative specific binding of four corresponding probes from the first, second, third and fourth probe sets;

(b) assigning a nucleotide in the sequence of the target nucleic acid as the complement of the interrogation position of the probe having the greatest specific binding;

(c) repeating (a) and (b) until each nucleotide of interest in the sequence of the target nucleic acid has been estimated.

14. (original) The method of claim 1, wherein the sequence of the target nucleic acid differs from the reference by at least two positions within a probe length.

15. (previously presented) A method of analyzing a target nucleic acid, comprising:

(a) designing an array of probes immobilized on at least one support based on an estimated sequence of the target nucleic acid, which has a sequence which is a variant of ~~the~~ a reference sequence, provided the array does not contain every possible probe sequence of a given length, whereby the probes of the array are complementary to and span the estimated target sequence,

(b) hybridizing the array of probes to the target nucleic acid;

(c) determining a reestimated sequence of the target nucleic acid from a hybridization pattern of the array to the target nucleic acid sequence to; and

(d) repeating (a)-(c) at least once with the designing step being based on the reestimated sequence of the target nucleic acid determined in step (c) of the previous cycle.